



results of BLAST

BLASTN 2.2.12 [Aug-07-2005]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1126736288-26655-34332709773.BLASTQ1

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
3,491,285 sequences; 15,298,534,039 total letters

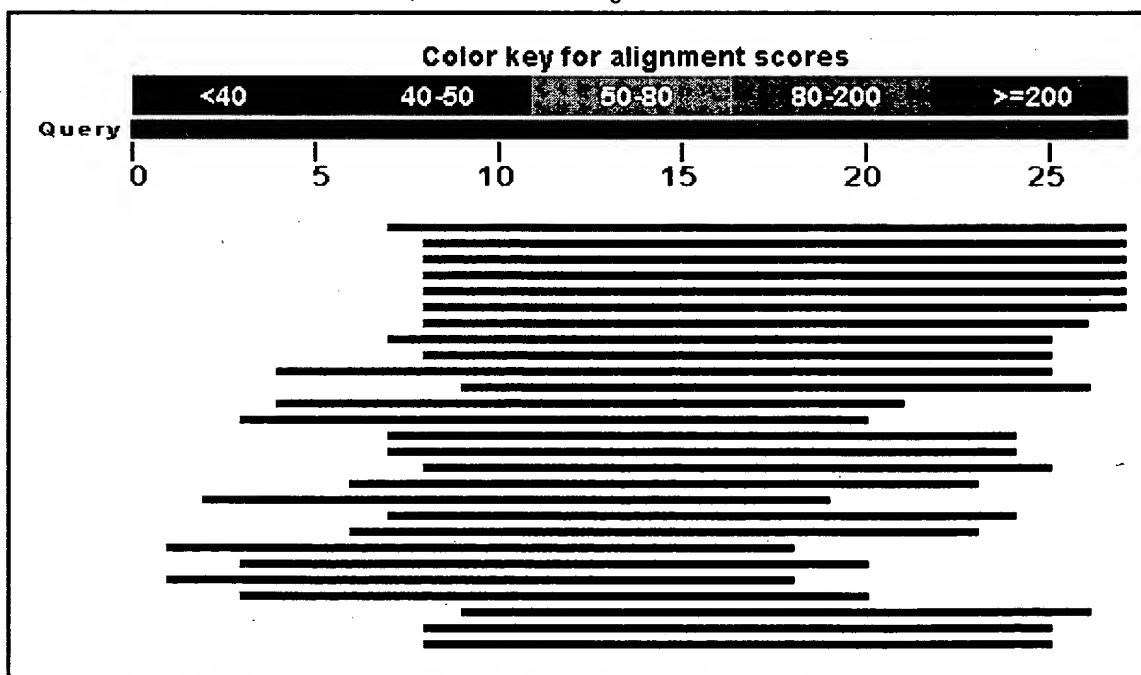
If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)
[Taxonomy reports](#)

Query=

(27 letters)

Distribution of 27 Blast Hits on the Query Sequence



Mouse over to see the define, click to show alignments



Sequences producing significant alignments:

Score E
(Bits) Value

BEST AVAILABLE COPY


gi 163282 gb M18780.1 BOVLACTBA	Bovine alpha-lactalbumin mRNA, c	40.1	0.10	
gi 46391243 gb AC147073.2	Pan troglodytes BAC clone RP43-169D10	38.2	0.40	
gi 2275186 gb AC002381.1	Homo sapiens BAC clone CTB-20D2 from 7	38.2	0.40	
gi 29294450 gb AC142331.1	Pan troglodytes BAC clone RP43-28J15	38.2	0.40	
gi 33235831 gb AC145774.1	Pan troglodytes BAC clone RP43-160F1	38.2	0.40	
gi 53386809 gb AC147976.3	Pan troglodytes BAC clone CH251-54...	38.2	0.40	
gi 49237636 emb BX897699.1	Bartonella henselae strain Houston-1	36.2	1.6	
gi 54633118 emb BX465862.7	Zebrafish DNA sequence from clone...	36.2	1.6	
gi 52627367 gb AE017354.1	Legionella pneumophila subsp. pneu...	34.2	6.2	
gi 71533370 gb AC154487.2	Mus musculus BAC clone RP24-119I4 ...	34.2	6.2	
gi 9105283 gb AE003895.1	Xylella fastidiosa 9a5c, section 41...	34.2	6.2	
gi 21537450 emb AL627095.8	Human DNA sequence from clone RP1...	34.2	6.2	
gi 16973165 emb AL603791.3	Human DNA sequence from clone RP1...	34.2	6.2	
gi 15591207 emb AL450243.13	Human DNA sequence from clone RP...	34.2	6.2	
gi 61966681 emb BX927163.31	Zebrafish DNA sequence from clon...	34.2	6.2	
gi 68131775 gb AC138596.13	Mus musculus chromosome 1, clone RP2	34.2	6.2	
gi 34482125 gb AC132619.3	Mus musculus BAC clone RP23-195N4 ...	34.2	6.2	
gi 23592205 gb AC122835.3	Mus musculus BAC clone RP23-187I18 fr	34.2	6.2	
gi 54110613 emb BX537142.10	Zebrafish DNA sequence from clon...	34.2	6.2	
gi 46848201 emb BX322623.7	Zebrafish DNA sequence from clone...	34.2	6.2	
gi 21629273 gb AC112175.2	Homo sapiens chromosome 5 clone CTD-2	34.2	6.2	
gi 45581130 emb AL928617.13	Mouse DNA sequence from clone RP...	34.2	6.2	
gi 16197757 gb AC008379.7	Homo sapiens chromosome 5 clone CTC-2	34.2	6.2	
gi 47118328 dbj BA000012.4	Mesorhizobium loti MAFF303099 DNA, c	34.2	6.2	
gi 28057550 gb AE012559.1	Xylella fastidiosa Temecula1, sec...	34.2	6.2	
gi 9930130 gb AF250324.1 AF250324	Homo sapiens chromosome 4q3...	34.2	6.2	
gi 56542470 gb AE008692.1	Zymomonas mobilis subsp. mobilis ZM4,	34.2	6.2	

Alignments

Get selected sequences


Select all

Deselect all

> ☐ gi|163282|gb|M18780.1|BOVLACTBA  Bovine alpha-lactalbumin mRNA, complete cds
Length=703

Score = 40.1 bits (20), Expect = 0.10
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Minus

Query 8 CAAATCAGGCTTTTATTCGG 27
|||||
Sbjct 703 CAAATCAGGCTTTTATTCGG 684

> ☐ gi|46391243|gb|AC147073.2|  Pan troglodytes BAC clone RP43-169D10 from 7, compl
Length=159447

Score = 38.2 bits (19), Expect = 0.40
Identities = 19/19 (100%), Gaps = 0/19 (0%)
Strand=Plus/Minus

Query 9 AAATCAGGCTTTTATTCGG 27
|||||
Sbjct 112937 AAATCAGGCTTTTATTCGG 112919